OIPE

RAW SEQUENCE LISTING   DATE: 12/28/2001
PATENT APPLICATION: US/09/942,936   TIME: 16:06:16

Input Set : A:\032301.205.seq.ST25.txt
Output Set: N:\CRF3\12282001\I942936.raw

ENTERED

```
 3 <110> APPLICANT: BATHE, Brigitte
 5 <120> TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE sigH GENE
 7 <130> FILE REFERENCE: 032301 WD 295
C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/942,936
C--> 9 <141> CURRENT FILING DATE: 2001-08-31
 9 <160> NUMBER OF SEQ ID NOS: 4
11 <170> SOFTWARE: PatentIn version 3.1
13 <210> SEQ ID NO: 1
14 <211> LENGTH: 1148
15 <212> TYPE: DNA
16 <213> ORGANISM: Corynebacterium glutamicum
18 <220> FEATURE:
19 <221> NAME/KEY: CDS
20 <222> LOCATION: (302)..(919)
21 <223> OTHER INFORMATION:
24 <400> SEQUENCE: 1
25 ttgttgatgg ctgtggctaa atcatcgtca tctttggggc gtaatcgatg ccaaaatgcg      60
27 aggtcacggc gattagtctc aacaatttcg gtgcttaaag gatcctgcgg attattgacg     120
29 gtgaagtaga acattgtttc cccctagatt tgaagtggta catatgttct aactgatgtg     180
31 gtggacacgc gggggtagag taaagtctaa gcaacagctc acgtggcttt acagctaccc     240
33 ccgaaaggtc tgttttttat cggaagtaga atagtcaaca cgcattttcg aaagggccaa     300
35 c atg gct gaa aac cga acc ggc aca gtc gat gga gac gcg ttg gct gcc     349
36   Met Ala Glu Asn Arg Thr Gly Thr Val Asp Gly Asp Ala Leu Ala Ala
37   1               5                   10                  15
39 cgc ttt gaa gag gag gca ctg cca ctc ctt gac cag ctc tat ggc ggt     397
40 Arg Phe Glu Glu Glu Ala Leu Pro Leu Leu Asp Gln Leu Tyr Gly Gly
41              20                  25                  30
43 gct ctg cgc atg act aga aat ccc gca gat gcg gaa gat ctc gtg caa     445
44 Ala Leu Arg Met Thr Arg Asn Pro Ala Asp Ala Glu Asp Leu Val Gln
45              35                  40                  45
47 gac acc tat atc aag gcg tac cag gcg ttc gcg agc ttc aaa cca ggc     493
48 Asp Thr Tyr Ile Lys Ala Tyr Gln Ala Phe Ala Ser Phe Lys Pro Gly
49      50                  55                  60
51 acc aac ctg aag gct tgg ctc tat cgg atc atg acg aat acc tac atc     541
52 Thr Asn Leu Lys Ala Trp Leu Tyr Arg Ile Met Thr Asn Thr Tyr Ile
53 65                  70                  75                  80
55 aac atg tac cga aag aaa cag agg cag cca tcg caa acc tct gcc gat     589
56 Asn Met Tyr Arg Lys Lys Gln Arg Gln Pro Ser Gln Thr Ser Ala Asp
57                  85                  90                  95
59 gag atc act gac tac cag ctc gtt gaa tct caa tcg cat acc tca aca     637
60 Glu Ile Thr Asp Tyr Gln Leu Val Glu Ser Gln Ser His Thr Ser Thr
61                  100                 105                 110
63 ggg ctg gaa tcc gcc gag gtt gag gct ctg aaa aat ctg cca gac gga     685
64 Gly Leu Glu Ser Ala Glu Val Glu Ala Leu Lys Asn Leu Pro Asp Gly
65              115                 120                 125
67 aaa att ggc gat gca atg aat caa ctc agc ccg gaa tac cgg atg gtg     733
68 Lys Ile Gly Asp Ala Met Asn Gln Leu Ser Pro Glu Tyr Arg Met Val
```

```
69      130                 135                 140
71 gtt tat tat gcc gat gta gaa gat ctc gca tac aaa gaa atc gcc gag      781
72 Val Tyr Tyr Ala Asp Val Glu Asp Leu Ala Tyr Lys Glu Ile Ala Glu
73 145                 150                 155                 160
75 atc atg gac gtt cca ctc gga act gtg atg tcc cga ctc cat cgt gga      829
76 Ile Met Asp Val Pro Leu Gly Thr Val Met Ser Arg Leu His Arg Gly
77                 165                 170                 175
79 aga aaa cag ctc cga gga atg tta aag gaa gta gcg aag gaa caa ggc      877
80 Arg Lys Gln Leu Arg Gly Met Leu Lys Glu Val Ala Lys Glu Gln Gly
81         180                 185                 190
83 att ggt ctt gaa cat ccc gac atg aag aaa aat tcg gag gca            919
84 Ile Gly Leu Glu His Pro Asp Met Lys Lys Asn Ser Glu Ala
85         195                 200                 205
87 taacgatgac gaatctcaac cgcagcgact cgcaaggtga ttgtggctgc cctgaattct      979
89 tcgatgaaat gtatcagcta ctcgacgatc aactcagcga gtccgcctgc gagcgtctgc     1039
91 ggattcacgc ggcaggctgc ccggcatgcc agcaactgct agaggccgaa tcggagtttc     1099
93 gtagtctgtt gcgcaagtgc tgctgcgaat cggcacctgt ggagctccg                1148
96 <210> SEQ ID NO: 2
97 <211> LENGTH: 206
98 <212> TYPE: PRT
99 <213> ORGANISM: Corynebacterium glutamicum
101 <400> SEQUENCE: 2
103 Met Ala Glu Asn Arg Thr Gly Thr Val Asp Gly Asp Ala Leu Ala Ala
104 1               5                 10                  15
107 Arg Phe Glu Glu Glu Ala Leu Pro Leu Leu Asp Gln Leu Tyr Gly Gly
108         20                  25                  30
111 Ala Leu Arg Met Thr Arg Asn Pro Ala Asp Ala Glu Asp Leu Val Gln
112         35                  40                  45
115 Asp Thr Tyr Ile Lys Ala Tyr Gln Ala Phe Ala Ser Phe Lys Pro Gly
116     50                  55                  60
119 Thr Asn Leu Lys Ala Trp Leu Tyr Arg Ile Met Thr Asn Thr Tyr Ile
120 65                  70                  75                  80
123 Asn Met Tyr Arg Lys Lys Gln Arg Gln Pro Ser Gln Thr Ser Ala Asp
124             85                  90                  95
127 Glu Ile Thr Asp Tyr Gln Leu Val Glu Ser Gln Ser His Thr Ser Thr
128         100                 105                 110
131 Gly Leu Glu Ser Ala Glu Val Glu Ala Leu Lys Asn Leu Pro Asp Gly
132         115                 120                 125
135 Lys Ile Gly Asp Ala Met Asn Gln Leu Ser Pro Glu Tyr Arg Met Val
136     130                 135                 140
139 Val Tyr Tyr Ala Asp Val Glu Asp Leu Ala Tyr Lys Glu Ile Ala Glu
140 145                 150                 155                 160
143 Ile Met Asp Val Pro Leu Gly Thr Val Met Ser Arg Leu His Arg Gly
144             165                 170                 175
147 Arg Lys Gln Leu Arg Gly Met Leu Lys Glu Val Ala Lys Glu Gln Gly
148         180                 185                 190
151 Ile Gly Leu Glu His Pro Asp Met Lys Lys Asn Ser Glu Ala
152         195                 200                 205
155 <210> SEQ ID NO: 3
```

RAW SEQUENCE LISTING   DATE: 12/28/2001
PATENT APPLICATION: US/09/942,936   TIME: 16:06:16

Input Set : A:\032301.205.seq.ST25.txt
Output Set: N:\CRF3\12282001\I942936.raw

156 <211> LENGTH: 28
157 <212> TYPE: DNA
158 <213> ORGANISM: Corynebacterium glutamicum
160 <400> SEQUENCE: 3
161 caggtacctt ttcgaaaggg gccacatg   28
164 <210> SEQ ID NO: 4
165 <211> LENGTH: 28
166 <212> TYPE: DNA
167 <213> ORGANISM: Corynebacterium glutamicum
169 <400> SEQUENCE: 4
170 tgtctagaaa gaattcaggg cagccaca   28

VERIFICATION SUMMARY   DATE: 12/28/2001
PATENT APPLICATION: US/09/942,936   TIME: 16:06:17

Input Set : A:\032301.205.seq.ST25.txt
Output Set: N:\CRF3\12282001\I942936.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date